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<b>(21) International Application Number:</b> PCT/GB96/03239 <b>(22) International Filing Date:</b> 24 December 1996 (24.12.96)  <b>(30) Priority Data:</b> 9526613.6 28 December 1995 (28.12.95) GB  <b>(71) Applicant (for all designated States except US):</b> NICKERSON BIOCEM LIMITED [GB/GB]; Cambridge Science Park, Milton Road, Cambridge CB4 4GZ (GB).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> TAYLOR, Mark, Andrew [GB/GB]; 9 Newhall Gardens, Dundee DD2 1TW (GB). DAVIES, Howard, Vivian [GB/GB]; 2 Station Road, Inver- gowrie, Dundee DD2 5DU (GB).  <b>(74) Agents:</b> CORNISH, Kristina, Victoria et al.; Kilburn & Strobe, 30 John Street, London WC1N 2DD (GB).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> POTATO ALPHA-GLUCOSIDASE GENE  <b>(57) Abstract</b>  The present invention provides recombinant or isolated nucleic acid encoding an $\alpha$ -glucosidase enzyme, especially those nucleic acid sequences encoding a plant $\alpha$ -glucosidase enzyme. Antisense nucleic acid is also provided, as well as the use of both the isolated or recombinant sequences and the antisense sequences. Uses of the invention include enhancing and reducing expression of $\alpha$ -glucosidases and the provision of novel starches.		

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## POTATO ALPHA-GLUCOSIDASE GENE

This invention relates to the fields of plant biotechnology and plant genetic engineering. In particular, it relates to the production of novel starches by plants and to the manipulation of starch-sugar conversions in transgenic plants by changing the cellular activity of the  $\alpha$ -glucosidase enzyme. More specifically, it relates to nucleic acid sequences encoding  $\alpha$ -glucosidase enzymes and the potential use of such sequences when expressed in plants.

It is known that the mobilisation of starch by hydrolysis in plants involves the enzymes  $\alpha$ -amylases,  $\beta$ -amylase, debranching enzyme and  $\alpha$ -glucosidase. However, the precise roles of the of starch degrading enzymes and their mechanisms of action remain unclear. One view is that  $\alpha$ -amylases are the only enzymes that use native starch as a substrate for hydrolysis. Accordingly, the role of  $\beta$ -amylase, debranching enzyme and  $\alpha$ -glucosidase is to hydrolyse the dextrins released by  $\alpha$ -amylase activity on the granule (reviewed by Beck and Zeigler, 1989). Conversely, some evidence suggests that  $\alpha$ -amylase cannot act on starch grains alone and requires other factors for starch degradation (Stamberg and Bailey, 1939). A good candidate for this  $\alpha$ -amylase activating factor is  $\alpha$ -glucosidase (Schwimmer, 1945). In fact some  $\alpha$ -glucosidases have been shown to catalyse the hydrolysis of soluble starch, although at very low rates (Yamasaki and Konno, 1985). In germinating barley there was a high degree of synergistic starch hydrolysis when  $\alpha$ -amylase and  $\alpha$ -glucosidase were incubated with starch granules (Sun and Henson, 1990). More recently, it has been demonstrated that a pea chloroplastic  $\alpha$ -glucosidase is capable of initiating chloroplastic starch grain degradation (Sun et al., 1995). This may cause starch grains to be more susceptible to further hydrolysis by

other enzymes. Thus, it appears that the importance of  $\alpha$ -glucosidases in starch hydrolysis may have been underestimated.

5         $\alpha$ -Glucosidases catalyse the hydrolysis or transfer of the terminal  $\alpha$ -D-glucosyl residues of  $\alpha$ -D-glucosidically linked carbohydrates. A general feature is that, unlike other starch degrading enzymes, a broad range of compounds are substrates for these enzymes.  
10        Generally, as well as catalysing the hydrolysis of maltose, they will also use oligosaccharides (maltodextrins) and polysaccharides (amylose, amylopectin and glycogen) as substrates (Yoshikawa et al., 1994). Additionally, most  $\alpha$ -glucosidases will hydrolyse a range  
15        of glucobioses containing  $\alpha$ -1,2,  $\alpha$ -1,3,  $\alpha$ -1,4 and  $\alpha$ -1,6 bonds. This may be particularly important if all these type of linkages are present in vivo, as other starch degrading enzymes such as  $\alpha$ -amylase cannot catalyse the breakdown of  $\alpha$ -1,2 and  $\alpha$ -1,3 bonds (Sun et al., 1995). Some evidence suggests that these types of  
20        linkages do exist in starch grains (Abdel-Akher, M. et al., 1952, Wolfrom and Thompson, 1956).  $\alpha$ -Glucosidases also catalyse transglycosylation reactions that may be important in vivo. For example, isomaltose, maltotriose  
25        and panose can be synthesised from maltose (Yamasaki and Suzuki, 1980, Yamasaki and Konno, 1985) and kojibiose, nigerose and maltose can be synthesised from soluble starch (Chiba, 1988).

30        It is well known that plants with novel characteristics can be produced by the expression of gene sequences introduced by transformation procedures such as *Agrobacterium*-mediated or vector mediated transformation methods or physical transformation methods such as

biolistics, chemical or electrical transfection or micro-injection, introducing genes or DNA sequences (Draper et al., 1988). Despite the widespread occurrence of  $\alpha$ -glucosidases in higher plants and their importance in starch and carbohydrate metabolism, no  $\alpha$ -glucosidase genes from plants have been characterised.

This has the disadvantage of preventing a transgenic approach for the manipulation of the expression of  $\alpha$ -glucosidase genes.

Accordingly, a first aspect of the present invention provides a recombinant or isolated nucleic acid encoding an  $\alpha$ -glucosidase enzyme, preferably a plant  $\alpha$ -glucosidase enzyme. Nucleic acid according to the present invention is preferably DNA but also includes cDNA and RNA. The  $\alpha$ -glucosidase enzyme of the present invention includes sequences which are preferably obtainable from plants or microbes including, in particular, the plants: potato, pea, maize, wheat, rice, barley, sweet potato, cassava or yam, amongst other species.

The present invention also includes, according to all aspects, mutations and fragments of nucleic acid sequences encoding  $\alpha$ -glucosidases (preferably  $\alpha$ -glucosidases obtainable from plants) and mutations and fragments of amino acid sequences of those  $\alpha$ -glucosidase enzymes. The present invention particularly includes nucleic acid and amino acid sequences of  $\alpha$ -glucosidase which are obtainable from the potato cultivars Record, Desiree, Binje or Russet Burbank as well as mutants and fragments thereof.

Fragments of nucleic acid according to the present

invention include 9 or more, preferably 12 or more, preferably 15 or more, preferably 18 or more bases and the corresponding number of amino acids. When used to describe the invention, the phrase 'a part of' means any size fragment thereof.

The recombinant or isolated nucleic acid according to the first aspect of the invention preferably encodes for an enzyme having the activity of a 105.4 kD  $\alpha$ -glucosidase enzyme of potato, especially the potato cultivar Record.

The recombinant or isolated nucleic acid nucleic acid according to the first aspect of the invention most preferably encodes at least part of (ie. a fragment of) the amino acid sequence as shown in Figure 2. The recombinant or isolated nucleic acid preferably encodes an amino acid sequence having more than 29% identity with the sequence shown in Figure 2, more preferably 40% identity, even more preferably 60% identity.

The recombinant or isolated nucleic acid may have a coding sequence operatively linked to a promoter. The promoter may be constitutive, for example the well known CaMV35S promoter or inducible, for example, the GAL/GAL10 promoter. The promoter may also be tissue-specific, for example, the tuber-specific promoter GBSSI, the tuber-specific patatin I promoter (Kim et al), the tomato fruit-specific E8 promoter (Lincoln et al) and the promoter of the small subunit of the ribulose-1,5-biphosphate carboxylase gene (Coruzzi et al).

According to a second aspect of the invention, there is provided a recombinant or isolated nucleic acid comprising a promoter which naturally drives expression

of a nucleic acid sequence encoding an  $\alpha$ -glucosidase enzyme, preferably a plant  $\alpha$ -glucosidase enzyme. The coding sequence for the  $\alpha$ -glucosidase is preferably as described above, according to the first aspect of the invention.

The recombinant or isolated nucleic acid according to the first and second aspects of the invention, when expressed, may result in enhanced starch and/or other carbohydrate breakdown, preferably in a plant. It may also result in novel starch structures. The enhanced breakdown is a result of increased expression of the  $\alpha$ -glucosidase enzyme, usually compared to endogenous levels. According to promoters used, for example, a tissue specific promoter, the increased levels of  $\alpha$ -glucosidase can be limited to desired tissues, such as plant storage organs (for example, potato tubers).

The recombinant or isolated nucleic acid of the first and second aspects of the invention may include a signal sequence in translational fusion with the  $\alpha$ -glucosidase coding sequence. Such a sequence may enable the expression of an introduced  $\alpha$ -glucosidase sequence specifically in a cellular organelle. For example, the GBSSI signal sequence targets expression to the plastid in potato tubers (Visser et al 1989).

According to a third aspect of the invention there is provided antisense nucleic acid to nucleic acid encoding  $\alpha$ -glucosidases of the present invention. Antisense nucleic acid is well understood in the art. Thus the present invention provides antisense nucleic acid which comprises a transcribable strand of nucleic acid, the transcribed nucleic acid being complementary to at

least part of a strand of nucleic acid which is transcribed from a nucleic acid sequence encoding a  $\alpha$ -glucosidase enzyme. Preferably, the nucleic acid sequence encoding the  $\alpha$ -glucosidase enzyme is obtainable from a plant, but it may also be obtainable from other sources, such as microbial sources (eg. yeast). The transcribable nucleic acid of the antisense and/or encoding the  $\alpha$ -glucosidase may be recombinant. The nucleic acid encoding the  $\alpha$ -glucosidase may be a 'natural' (endogenous) nucleic acid sequence (which may also be recombinant) or may be a modified sequence. The nucleic acid encoding the plant  $\alpha$ -glucosidase enzyme may be obtainable from a potato, in particular, the potato cultivar Record. The nucleic acid encoding the plant  $\alpha$ -glucosidase enzyme may preferably encode for an enzyme having the activity of a 105.4 kD  $\alpha$ -glucosidase enzyme of potato.

The antisense nucleic acid is advantageously complementary to part of a nucleic acid sequence encoding for the amino acid sequence shown in Figure 2. Preferably the antisense nucleic acid is complementary in the same level of identity as described hereinbefore for the recombinant or isolated nucleic acid. In this way, the transcribable strand of nucleic acid from the antisense nucleic acid will be complementary to at least part of the strand of the nucleic acid which is transcribed from the nucleic acid encoding a plant  $\alpha$ -glucosidase enzyme.

The antisense nucleic acid may be operatively linked to a promoter, as described according to the first aspect of the invention.



According to a fourth aspect of the invention there is provided nucleic acid capable of disrupting the proper expression of an  $\alpha$ -glucosidase gene, preferably a plant  $\alpha$ -glucosidase gene, most preferably an  $\alpha$ -glucosidase gene of potato, pea, maize, wheat, rice, barley, sweet potato, cassava or yam. The disruption may be by any recombinant nucleic acid technology, including those well known in the art. The nucleic acid capable of the most effective disruption, disrupts proper expression of a gene encoding an  $\alpha$ -glucosidase enzyme having the activity of a 105.4 kD  $\alpha$ -glucosidase enzyme of potato. Nucleic acid capable of disrupting the proper expression of an  $\alpha$ -glucosidase gene, according to the invention, may comprise nucleic acid obtainable from a source other than a plant eg. a microbial source, in particular a yeast.

The nucleic acid according to any aspect of the invention may comprise a 5' transcription regulation sequence such as the 5' transcription regulation sequence derived from the Cauliflower Mosaic Virus 35S gene, GBSSI, patatin, E8 and the promoter of the RUBISCO small subunit gene.

Nucleic acid, according to any aspect of the invention may comprise part of a vector. Suitable vectors are well known in the art and include cloning vectors such as lambda Zap II (Stratagene) and expression vectors such as pYES2 (Invitrogen). Preferably, the vector comprises one or more selectable markers such as antibiotic resistance.

A construct, comprising nucleic acid according to any one of the aspects of the invention, and including the vectors according to the invention can be introduced into a host cell by transfection or transformation. Such methods are well known in the art. The host cell can

than be used to express and monitor expression of  $\alpha$ -glucosidase activity or can be used to clone plants, microbes and/or parts of plants, including tissue culture.

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Preferably, a construct comprising a promoter operatively linked to a nucleic acid sequence, encoding an  $\alpha$ -glucosidase enzyme can be transformed into a plant or other organism, such as a microbe, eg. yeast. Suitable plants include potato, pea, maize, wheat, rice, barley, sweet potato, cassava or yam amongst others. Suitable transformation techniques are well known in the art as described above. The transformation results in plants, or other organisms, at least some of the cells of which contain a foreign chimeric nucleic acid sequence composed of a promoter operatively linked to nucleic acid encoding an  $\alpha$ -glucosidase enzyme. These constructs can include nucleic acid encoding any  $\alpha$ -glucosidase (eg. plant, or microbial) for introduction into plant, microbial or animal cells.

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In this way, the nucleic acid of the present invention can be used to modify starch and/or other carbohydrate breakdown in material, in particular in plant material. Clearly, the most effective use of such systems are when the promoter sequence drives preferential expression of the nucleic acid in plant storage organs and/or seeds. As a result, the rate of starch and/or other carbohydrate breakdown in plant materials can be modified as well as the potential to produce novel starches and/or other carbohydrates in plants, preferably plant storage organs.

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The nucleic acid sequences, constructs, vectors etc., according to the first aspect of the invention, can be

used to obtain enhanced  $\alpha$ -glucosidase activity in plant or other organisms material/tissues. A consequence of this is a more efficient breakdown of starch and/or other carbohydrates and the opportunity to product novel starches and/or other carbohydrates. This is a benefit to processes which lead to the production of glucose and/or other starch derived products such as maltose and maltose oligosaccharides. These includes the malting and brewing process in which the efficiency of starch conversion to glucose will be increased, leading to increased spirit yield. Additionally, increased starch breakdown will increase the glucose content of plant tissues and will consequently enhance the flavour characteristics of plant tissues (for example the fruit of tomato, strawberry, raspberry, blackcurrent).

Furthermore, the nucleic acid sequences, constructs, vectors, etc., according to the third and fourth aspects of the invention can be used to obtain reduced  $\alpha$ -glucosidase activity in plant or microbial material. Inhibition of  $\alpha$ -glucosidase activity by transformation of plant tissue with constructs containing the potato  $\alpha$ -glucosidase sequence in antisense orientation will result in inhibition of starch breakdown in seeds and other storage organs. This will be of use in developing tissues, in storage tissue and in germinating systems. Applications also include inhibition of pre-sprouting in cereals, sprout control in potato, minimising starch and dry weight losses in storage and during cooking or processing. A potential outcome is restricted starch turnover rates and a subsequent increase in the amount of starch deposited.

The nucleic acid sequences of the present invention can

be used as hybridisation probes to clone  $\alpha$ -glucosidase genes from other sources and species, for example microbes and pea, maize, wheat, rice, barley, sweet potato, cassava and yam (respectively).

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A further aspect of the present invention also provides for novel starch structures, in particular in plant materials. The novel starches are a result of the  $\alpha$ -glucosidase activity at differing levels and/or from differing sources. The novel starch structures may have a changed branched structure and/or a changed branch length.

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The invention is illustrated by the accompanying drawings in which:

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Figure 1. shows the nucleotide sequence of the coding strand of the potato cultivar Record cDNA that encodes  $\alpha$ -glucosidase.

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Figure 2. shows the deduced amino acid sequence from the cDNA sequence in Figure 1.

Figure 3. shows a comparison of the deduced amino acid sequence of the potato  $\alpha$ -glucosidase (labelled pot) with that of the human lysosomal sequence (labelled hum). The comparison was carried out using the default parameters of the GAP programme of the GCG package.

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Figure 4. shows growth of yeast strains. (o) non-transformed ABYSMAL81 with 2% glucose as carbon source, (●) ABYSMAL81 transformed with pMAL1YES2 with 0.1% galactose and 2% maltose as carbon source, (□) ABYSMAL81 with 0.1% galactose and 2% maltose as carbon source and

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(■) ABYSMAL81 transformed with pYES2 with 0.1% galactose and 2% maltose as the carbon source.

5 Figure 5. shows  $\alpha$ -glucosidase activity in crude extracts of ABYSMAL81 transformed with pMAL1YES2 measured in the pH range 3-9.

The invention is illustrated by the following non-limiting examples.

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*Example 1*

*Isolation and sequence analysis of a potato  $\alpha$ -glucosidase clone.*

15 An *Arabidopsis* expressed sequence tag (EST) (European Molecular Biology Laboratory (EMBL) accession number; t04464.em\_est) with sequence similarity to the human lysosomal  $\alpha$ -glucosidase gene (Hoefsloot et al., 1988) was used as a probe to obtain the corresponding potato  
20 cDNA (pMAL1). The EST was generated in an *Arabidopsis* expressed sequence project and can be accessed as described in Newman et al., 1994. A potato cDNA (cultivar Record) library constructed in Zap II (Stratagene) from tuberising stolon tip mRNA (Taylor et al., 1992) was  
25 screened by standard techniques using this EST as a probe. Following in vivo excision and sub-cloning, DNA sequence of the pMAL1 clone was obtained for both strands using cycle sequencing (DyeDeoxy Terminator kit, Perkin Elmer) and a 373 automated DNA sequencer (Applied  
30 Biosystems). DNA sequence analysis was carried out using software available on the SEQNET Computational Molecular Biology Facility at SERC Daresbury Laboratory UK. The size of the insert in the pMAL1 was 2992bp (Fig. 1). An open reading frame from the nucleotide in position 62 to

a termination codon at position 2819 was identified. The sequence around the putative ATG initiation codon (A at position 51) is AACCATGA and shares some similarity with the preferred context for higher eukaryotes (CACCATGG, Kozak, 1987). The polypeptide encoded by this ORF has a molecular weight of 105.4 kD and an isoelectric point of 5.75. The deduced amino acid sequence of the *pMAL1* open reading frame was compared with sequences in the EMBL database. The most significant matches were with members of family 31 of glucosyl transferases which includes  $\alpha$ -glucosidases from human (Hoefsloot et al., 1988) and *Candida tsukubaensis* (Kinsella et al., 1991). The most similar full length sequence was that of a human lysosomal  $\alpha$ -glucosidase (Hoefsloot et al., 1988, Fig 2). Overall the sequences share 50% similarity and 29% identity. The two sequences were less similar in the amino-terminal portion (41% similarity, 16% identity over the first 280 amino acids) however over the remaining portion of the sequence there is 53% similarity and 34% identity. Clusters of identical amino acids occur throughout this region. One of the most highly conserved regions is adjacent to the aspartic acid residue at amino acid 516 of the potato sequence. Regions highly similar to this are at the active site of rabbit isomaltase and sucrase (Hunziker et al 1986). The *pMAL1* ORF was also compared with the deduced amino acid sequences of ESTs from *Arabidopsis*, rice and *C.elegans* that show similarity to  $\alpha$ -glucosidases. The *pMAL1* ORF shared 77%, 76% and 58% identity, respectively with these sequences (not shown).

#### Example 2

Complementation of a yeast  $\alpha$ -glucosidase mutant.

To confirm that the *pMAL1* clone did encode a functional  $\alpha$ -glucosidase gene, its ability to complement an  $\alpha$ -glucosidase-negative mutant strain of *Saccharomyces cerevisiae* was investigated. Such a mutant strain of *Saccharomyces cerevisiae* designated ABYSMAL81 (Kopetzki et al., 1989) has the genotype *ura3-52mal1S-<sup>+</sup>pralprblprclcpsllys*. This mutant was used in transformation studies using standard yeast culture and manipulation methods as described by Rose et al., 1990.

The open reading frame encoding the potato  $\alpha$ -glucosidase was cloned into the *Hind* III site of the yeast expression vector *pYES2* (Invitrogen) to generate the construct *pMAL1YES2* using standard techniques. The coding region of the cDNA clone was amplified using the Expand High Fidelity PCR system (Boehringer Mannheim) and the sequence of the PCR product was verified. PCR primers were designed to incorporate *Hind* III sites at the 5' and 3' termini of the fragment and the initiation codon was preceded by an AT rich sequence (TTAAA) in order to enhance efficient translation initiation (Romanos et al., 1995). The sequence of the primers used for building the yeast expression construct containing the amplified potato  $\alpha$ -glucosidase sequence were:

5' primer: cgaagcttaaaatgagagctccactactc  
3' primer: cccaagcttgaatcgaccaatcatc

The lithium acetate transformation method (Rose et al., 1990) was used to introduce the plasmids *pYES2* and *pMAL1YES2* independently into the yeast strain ABYSMAL81. Transformants were selected for uracil auxotrophy by standard procedures. Expression of the *MAL1* sequence in the *pMAL1YES2* construct was under the control of the *GAL1* portion of the *GAL1/GAL10* promoter which is inactive in

the absence of galactose, induced a 1000 fold in its presence and is subject to glucose repression (Johnston, 1987). Growth of *pMAL1YES2* transformants was observed in the presence of 0.1% galactose and 2% maltose at a rate similar to that of the non-transformed mutant and vector transformed mutant growing on 2% glucose as the carbon source (Fig. 4). It was confirmed that the non-transformed mutant and vector transformed mutants were incapable of growth on this maltose/galactose medium and the transformant required the addition of galactose for growth. Presumably the level of galactose in the medium (0.1%) was too low to support growth of the mutant but was sufficient to induce expression from the *GAL1* promoter.

$\alpha$ -Glucosidase activity in crude yeast extracts was determined in the transformed and non-transformed mutant strains. Overnight cultures of yeast (50 ml) were harvested by centrifugation (2000g, 5 min) and the cell pellet resuspended in 0.5 ml of 10 mM sodium phosphate buffer, pH 6.5. Cells were broken by sonication using a Misonix Ultrasonic Cell Disruptor (Misonix Inc) and cell debris was then sedimented by centrifugation (16000g, 20 min). Small molecules were removed from the supernatant by gel filtration using a PD-10 Sephadex G-25 M column (Pharmacia).  $\alpha$ -Glucosidase activity was determined using a range of maltodextrins, amylopectin and boiled soluble starch as substrates. The reaction mixture (100 L) contained 50mM maltodextrin or 2% (w/v) amylopectin or boiled soluble potato starch substrate in sodium phosphate buffer pH 6.5, and 50  $\mu$ L of crude extract and was incubated for 1 hour at 30°C. The reaction was terminated by boiling for 5 minutes and the amount of glucose released determined by the reduction of  $\text{NAD}^+$  in



the coupled reactions of hexokinase and glucose-6-phosphate dehydrogenase in the presence of ATP and NAD<sup>+</sup> in a microtiter plate assay (Viola and Davies, 1992). Significant activity was detected following transformation of the *ABYSMAL81* mutant with *pMALIYES2* and galactose induction. No activity could be detected in the non-transformed or *pYES2* transformed *ABYSMAL81* strain (Table 1). The optimum pH for  $\alpha$ -glucosidase activity was 6.5 (Fig.5).

The rate of hydrolysis of a range of maltodextrins, amylopectin, and boiled starch was also investigated (Table 1). The greatest activity was observed when maltotetraose was the substrate (151% of the maltose rate). Very little activity (5% of the maltose rate) was detected when amylopectin or boiled soluble starch were used as substrates although this was significantly greater than in the non-transformed mutant.

Table 1.  $\alpha$ -Glucosidase activity in crude extracts of ABYSMAL81 transformed with pMAL1YES2. The 100% maltose rate was 3.25 nmoles glucose/ g protein / hr.

5	<b>Substrate</b>	<b><math>\alpha</math>-glucosidase activity. (percentage of maltose rate)</b>
	maltose	100
	maltotriose	142
10	maltotetraose	151
	maltopentaose	117
	maltohexaose	68
	maltoheptaose	50
	amylopectin	5
15	boiled starch	5

### Example 3

#### *Transformation studies.*

Preliminary transformation studies were carried out using  
 20 constructs containing the potato *MAL1* sequence. Two  
 constructs were built as described below. An antisense  
 construct containing the entire *MAL1* coding sequence in  
 reverse orientation under the control of two copies of  
 the constitutive CaMV 35S promoter and containing the nos  
 25 terminator was cloned into the plant transformation  
 vector pBIN19 (Bevan, 1984). This vector contained a  
 kanamycin selection marker. A sense construct was built  
 as above except the entire *MAL1* coding region was cloned  
 in the sense orientation. 59 independent (determined by  
 30 Southern analysis (Sambrook et al., 1989)) transgenic  
 potato antisense lines and 45 sense lines were generated  
 in the potato cultivar Desiree following standard  
 transformation protocols (Kumar, 1995).

## Example 4

 *$\alpha$ -Glucosidase activity measurements.*

$\alpha$ -Glucosidase activity measurements were carried out (Cochrane et al., 1991) on tuber and leaf samples from the *MAL1* antisense plants in Example 3. In tubers from these transgenic lines, a small (20%) but consistent decrease in activity was detected on either a protein or fresh weight basis in three lines. In leaf samples from the antisense lines a significant decrease in activity was measured, in some lines the activity was approximately 50% that observed in vector-only transformed leaves. Other lines showed a decrease in activity of up to 50%.

## Example 5

*Tuber sugar content.*

Glucose, fructose and sucrose were assayed by high pH anion exchange chromatography with pulsed amperometric detection using a CarboPac PA-100 column following the manufacturer's protocol (Dionex) in samples of tissue from "first generation" transgenic tubers (tubers stored for three months at 4°C) (the antisense plants from Example 3). Compared with transgenic plants transformed with only the vector (pBIN19), a decrease in sucrose content was measured in some transgenic *MAL1* antisense lines (table 2 below). In the line that exhibited the strongest effect, sucrose levels were approximately 30 to 60% of the control values.

Table 2. Levels of glucose, fructose and sucrose in stored potato tubers from *MAL1* antisense plants compared with those from vector-only transformed plants.

(Data from selected lines to show range of values

obtained in antisense plants, values for antisense plants mean of 5 replicates from different tubers of the same transgenic line or mean of 8 replicates for the vector-only transformed control.)

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	Transgenic line	glucose	fructose	sucrose
		mg glu/gfr.wt.	mg fru/gfr.wt.	mg glu/gfr.wt.
	2M1	0.05	0.05	1.08
10	3M4	0.09	0.08	1.74
	11E	0.19	0.28	0.84
	12C	0.05	0.08	1.17
	12D	0.10	0.13	1.10
	control	0.08	0.11	1.89

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#### Example 6

*Leaf starch turnover, maltose content and  $\alpha$ -glucosidase activity.*

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The rate of starch turnover in fully expanded leaves from selected lines of antisense *MAL1* plants (from Example 3) was measured. Plants were grown in a growth cabinet at saturating light intensities with an 18 hour light period and a six hour dark period. Starch was extracted from leaves (Leidreiter et al. 1995) at the end of the light period and after four hours of darkness. The ratio of starch content in the light and dark was found to be consistently higher in the vector-only transformed lines (mean value 3.3) compared with the *MAL1* antisense lines (lowest values 2.4). The maltose content after 4 hours of darkness was also measured in leaf samples. Leaves from the *MAL1* antisense lines had up to twice the maltose content of those from vector-only transformed control lines. The results are shown in Table 3.

Table 3.

Starch content,  $\alpha$ -glucosidase activity and maltose levels in leaves from *MAL1* antisense plants and vector-only transformed plants (control) after 18 hours light treatment (L) and 4 hours dark treatment (D). Data represent mean values of 5 samples.

Transgenic line	$\alpha$ -glucosidase activity (vector value = 100%)	maltose	starch content	ratio (L/D)	
				mM glu/gfr.wt light	dark
control	100	100	46.4	14.4	3.20
3M4	63	200	43.4	18.4	2.36
11E	54	204	50.2	19.2	2.60
14A	76	143	55.7	24.3	2.29

#### Example 7

##### *Targetted expression of the MAL1 gene.*

A construct has been designed in which the expression of the *MAL1* gene is under the control of the tuber-specific GBSSI promoter (Visser et al., 1989). The construct also contains the GBSSI targetting sequence so that the *MAL1* gene product was targetted to the amyloplast. Plants have been transformed with this construct and the *MAL1* gene product was expressed preferentially in the amyloplast.

##### *Summary of the Transformation Studies.*

Approximately 50 transgenic lines containing the *MAL1* sequence in sense and antisense orientation have been generated. In leaf samples of the antisense lines,

$\alpha$ -glucosidase activity was reduced by up to 50% compared with the vector control values. In tubers, few lines exhibited a consistent decrease in maltase activity and there was considerable tuber to tuber variability. Two  
5 consistent effects have been noticed however. Firstly, starch turnover rate (as determined by the ratio of light to dark starch content) was significantly lower in leaves from some *MAL1* antisense lines. Maltose levels in leaves from these antisense plants were higher (up to double  
10 that routinely measured in leaf samples from control plants). Secondly, in stored tubers from the antisense lines, the sucrose level was consistently lower than in control tubers, in some lines the sucrose content was only 30 to 60% of that observed in the control tubers.

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30

**CLAIMS**

1. Recombinant or isolated nucleic acid encoding an  $\alpha$ -glucosidase enzyme, preferably a plant  $\alpha$ -glucosidase enzyme.
- 5 2. Recombinant or isolated nucleic acid as claimed in claim 1 which is obtainable from potato.
- 10 3. Recombinant or isolated nucleic acid as claimed in claim 2 which is obtainable from the potato cultivar Record.
- 15 4. Recombinant or isolated nucleic acid, as claimed in any one of claims 1 to 3, wherein the enzyme has the activity of a 105.4 kD  $\alpha$ -glucosidase enzyme of potato.
- 20 5. Recombinant or isolated nucleic acid as claimed in any one of claims 1 to 4 encoding at least part of the amino acid sequence as shown in Figure 2.
- 25 6. Recombinant or isolated nucleic acid as claimed in any one of claims 1 to 5, wherein a coding sequence is operatively linked to a promoter.
- 30 7. Recombinant or isolated nucleic acid comprising a promoter which naturally drives expression of a nucleic acid sequence encoding a plant  $\alpha$ -glucosidase enzyme.
8. Recombinant or isolated nucleic acid as claimed in claim 7, wherein the coding nucleic acid sequence is as claimed in any one of claims 1 to 7.
9. Recombinant or isolated nucleic acid as claimed in any claim 6 to 8 which, when expressed, results in

enhanced starch and/or other carbohydrate breakdown in a plant or microbe.

- 5 10. Recombinant or isolated nucleic acid as claimed in any one of claims 6 to 9 including a signal sequence in translational fusion with the  $\alpha$ -glucosidase coding sequence
- 10 11. Antisense nucleic acid which comprises a transcribable strand of nucleic acid, which is complementary to at least part of the strand of nucleic acid which is transcribed from a nucleic acid sequence encoding a  $\alpha$ -glucosidase enzyme, preferably a plant  $\alpha$ -glucosidase enzyme.
- 15 12. Antisense nucleic acid as claimed in claim 11 wherein the sequence encoding the  $\alpha$ -glucosidase enzyme is obtainable from potato.
- 20 13. Antisense nucleic acid as claimed in claim 12, wherein the sequence encoding the  $\alpha$ -glucosidase enzyme is obtainable from the potato cultivar Record.
- 25 14. Antisense nucleic acid as claimed in claim 13, wherein the  $\alpha$ -glucosidase enzyme has the activity of a 105.4 kD  $\alpha$ -glucosidase enzyme of potato.
- 30 15. Antisense nucleic acid as claimed in any one of claims 11 to 14 which is complementary to at least part of the nucleic acid sequence encoding the amino acid sequence as shown in Figure 2.
16. Antisense nucleic acid as claimed in any one of claims 11 to 15 operatively linked to a promoter.

17. Nucleic acid capable of specifically disrupting the proper expression of an  $\alpha$ -glucosidase gene, preferably a plant  $\alpha$ -glucosidase gene.
- 5 18. Nucleic acid as claimed in claim 17, wherein the  $\alpha$ -glucosidase gene encodes a 105.4 kD  $\alpha$ -glucosidase enzyme of potato.
- 10 19. Nucleic acid as claimed in any one of claims 1 to 18 comprising a 5' transcription regulation sequence.
- 15 20. Nucleic acid as claimed in claim 19, wherein the 5' transcription regulation sequence is derived from the Cauliflower Mosaic Virus 35S gene.
21. Nucleic acid as claimed in any one of claims 1 to 20 which is recombinant and comprises part of a vector.
- 20 22. Nucleic acid as claimed in claim 21, wherein the vector is a cloning or an expression vector and comprises one or more selectable markers.
- 25 23. A host cell transfected or transformed with a vector as claimed in claim 21 or claim 22.
24. A plant or microbial cell comprising nucleic acid as claimed in any one of claims 1 to 10 or 19 to 23 (when dependent on any one of claims 1 to 10).
- 30 25. A plant or microbial cell comprising nucleic acid as claimed in any one of claims 11 to 18 or 19 to 23 (when dependent on any one of claims 11 to 18).
26. A plant, microbe, or part of a plant, at least some

of whose cells are as claimed in claim 24.

27. A plant, microbe, or part of a plant, at least some of whose cells are as claimed in claim 25.

5

28. Use of nucleic acid as claimed in any one of claims 1 to 22 to modify starch and/or other carbohydrate breakdown in plant or microbial material.

10

29. Use of nucleic acid as claimed in any one of claims 1 to 10 or 19 to 23 (when dependent on any one of claims 1 to 10) to obtain enhanced  $\alpha$ -glucosidase activity in plant or microbial material.

15

30. Use of nucleic acid as claimed in claim 29 to enhance flavour characteristics of plant tissue.

31. Use of a plant, or part of a plant, as claimed in claim 24 in a malting or brewing process.

20

32. Use of nucleic acid as claimed in any one of claims 11 to 18 or 19 to 23 (when dependent on any one of claims 11 to 18) to obtain reduced  $\alpha$ -glucosidase activity in plant or microbial material.

25

33. Use of nucleic acid as claimed in claim 32 to control pre-sprouting in cereals, sprout control in potato or loss of starch and/or dry weight in storage, cooking or processing of plant material.

30

34. A novel starch structure obtainable by expression of nucleic acid as claimed in any one of claims 1 to 22.

1 / 6

1	CGACGGCCAGTGAATTCCGGTCTTCTATGATATCTTCCACATTGATCTCCGATTATAAC	60
61	CATGAGAGCTCCACTACTCCTATATCCACTCCTTCTCCTCCTTCTATTTGTTACCTCTGC	120
121	CTACTCCTGGAAGAAGGAGGAGTTTCGAAACTGCGACCAAACCCCATTTTGCAAAAGAGC	180
181	CCGTCCCCGAAAACCTGGATCGTGCAATCTGCGGGTTGCCGATGTGTCCATCTCCGATGG	240
241	GGATCTTATAGCCAAACTTGTCCCCAAGAAGAAAACCCAGAAAGTGAACAACCCAATAA	300
301	GCCTTTGGTTCTCACTCTTTCTGTGTACCAAGATGGTGTGATGAGGGTGAAAATTGATGA	360
361	AGATCAAAATCTGAATCCACCCAAGAAAAGATTTGAAGTTCCTGAGGTGATTGAGGAAGA	420
421	TTTCCTCAACACCAAGCTGTGGTTAACAGAGTAAAAGAGGAGCAAATCGACGGAGTTTC	480
481	GAGTTTTTCCTCTGTTTTTTACTTGTCTGATGGGTATGAAGGGGTGTTGAGACATGACCC	540
541	ATTTGAGGTTTTGGCAGAGAGAGTGAAGTGGGAAGAGAGTGTGTCCATAAACTCAAA	600
601	TGGGTTGTTTGATTTTGAACAGTTGAGGGAGAAGAAAGAGGGGATGATTGGGAGGAGAA	660
661	GTTTAGGAGTCATACTGATACAAGGCCTTATGGTCCACAATCAATTAGTTTTGATGTATC	720
721	TTTTTATGGTGCAGATTTTGTATGGCATTCTGAACATGCTACTAGTTTTGCTTTGAA	780
781	ACCAACTAAGGGGCCTAATGTAGAGGAATATTCGAGCCTTATAGGTTATTTAATCTTGA	840
841	TGTGTTTGAGTATCTTCATGAGTCGCCCTTTTGGGCTTTATGGTTCAATTCCTTTTCATGAT	900
901	GGACATGGGAAAAGCCAGGGGTAGTTCGGGTTTTTTCTGGTTGAATGCTGCGGAATGCA	960
961	GATTGATGATTGGGATCTGGTTGGAATTCAGATGAGTCTTCAAAGATAATGTTGCCCTC	1020
1021	GGACAAGCACAGGATTGATACTTTATGGATGAGTGAGTCTGGTGTAGTGGATACGTTCTT	1080
1081	TTTCATTGGTCTCGGGCCAAAAGATGTGGTTAGGCAGTATACTAGTGTAAACGGGAAGGCC	1140
1141	ATCTATGCCACAGTTATTTCGCAACTGCATACCATCAATGTAGATGGAATTATAGAGACGA	1200
1201	GGAAAGATGTTTATAATGTTGATTCAAAATTTGATGAGCATGATATCCCTTATGATGTTTT	1260
1261	GTGGCTTGATATTGAGCACACAGATGGGAAGAAGTACTTTACTTGGGACAGGGTGTTATT	1320
1321	TCCTAACCCGGAAGAAATGCAGAAGAAGTTAGCTGCAAAGGGTAGACACATGGTTACCAT	1380
1381	TGTGGATCCTCATATCAAGAGGGATGAGTCTTACCATATACCCAAGGAGGCCTTAGAAAA	1440
1441	GGGATACTATGTTAAGGATGCTACTGGTAAGGATTATGATGGATGGTGTGGCCTGGTTC	1500
1501	CTCATCATATACTGACTTGCTGAATCCCGAGATTAAAGTCATGGTGGAGTGACAAATTTTC	1560
1561	ACTTGATAGCTATGTTGGCTCAACAAAGTATTTATACATCTGGAATGACATGAATGAACC	1620
1621	TTCCGTCTTCAATGGACCAGAGGTAACAAATGCCAAGAGATGCTTTACATCATGGAGGAGT	1680
1681	AGAGCACAGGGAGTTGCACAATTCATATGGTTACTATTTCCATATGGGAACATCCGACGG	1740
1741	GCTTCTAAAGCGTGGAGATGGAAAAGATAGGCCCTTTGTTTTGGCAAGGGCCTTCTTTGC	1800
1801	CGGAAGTCAAAGATATGGAGCAATTTGGAGTAAAGTAAATACAGCAGAATGGGAGCACTT	1860
1861	GAGGGTTTTAGTCCCCATGGTGTAACTCTTAGCATCTCTGGAATAGTATTTTCTGGTGC	1920
1921	AGATGTTGGTGGATTTTTTGGTAATCTGACACTGAGTTGTTGGTTCGCTGGTATCAAGT	1980
1981	AGGTGCATATTATCCCTTTTTCCGGGGCATGCACATCATGACACTAAAAGACGGGAACC	2040
2041	TTGGTTATTTGGAGAAAGAAATACACAATTGATGAGGGAAGCGATACATGTTTCGTTACAT	2100
2101	GTATCTTCCTTATTTCTACACTCTATTTAGAGAAGCAAATTCAAGTGGTACTCCAGTTGC	2160
2161	TCGCCCCACTTTGGATGGAGTTCCTGGAGACGAAAAATCTTTTAGCAATGATGAGGCTTT	2220
2221	CATGGTTGGGAATGGTCTTCTAGTGCAAGGAGTTTATACAGAGAAACCAAACATGTTTC	2280
2281	TGTCTATCTACCAGGGGAGGAATCCTGGTATGATTTAAGAAGTGCATCTGCATACAACGG	2340
2341	AGGTCATACACACAAGTATGAGGTTTCAGAAGATAGTATTCCTTCTTTTCAAAGGGCCGG	2400
2401	AACTATCATACCAAGGAAAGATCGTTTACGTCCGAGCTCGACACAGATGGAAAATGATCC	2460
2461	TTATACTCTGGTTATAGCTCTTAATAGTTCCAAGGCAGCTGAAGGTGAGCTTTATATCGA	2520
2521	TGATGGGAAGAGCTATGAGTTCAAACAAGGTGCCTTCATTCTCAAATGGGAGGCTTATAT	2580
2581	CTTCCAAATGCAGCCCCGTCTACAGCTGGCAGTGACACATTTTCCTTCCGAGTGCATGT	2640
2641	AGAGAGGATAATCTTGTAGGATTGTCTCCTGGAGCTAAAACAGCCCTTATTGAACCAGG	2700
2701	AAACAAGAAAGTTGAAATTGAGCTTGGGCCACTCTTCATTCAAGGAAATCGAGGATCTGT	2760
2761	TCCAACCATCCGCAAGCCTAATGTGCGTATTACAGATGATTGGTCGATTCAAATTTTGTA	2820
2821	AGAAGTTGGTAGTTATGACGAAGTCTTACATTTTCTCTCCGCTTCATCATGTATTGG	2880
2881	GTTAGACCAGCTAATAGGTAAATCTTTACTAGAAGAATTAACATTGATGAAGATTGTTA	2940
2941	TACAGGGATAGTTGAAGCGGCCGCAATTCGAGCTCGGTACCCGGGGATCC	2992

FIG. 1.

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1 MRAPLLLYPL LLLLLFVTSY YSWKKEEFRN CDQTPFCKRA RSRKPGSCNL  
51 RVADVSISDG DLIAKLVPKE ENPESEQPNK PLVLTLSVYQ DGVMRVKIDE  
101 DQNLNPPKKR FEVPEVIEED FLNTKLWLTR VKEEQIDGVS SFSSVFYLSL  
151 GYEGVLRHDP FEVFARESGS GKRVLSSNSN GLFDLFEQLRE KKEGDDWEEK  
201 FRSHTDTRPY GPQSSSFDVS FYGADFVYGI PEHATSFALK PTKGPNVEEY  
251 SEPYRLFNLN VFEYLHESPF GLYGSIPFMI SHGKARGSSG FFWLNAAEMQ  
301 IDVLGSGWNS DESSKIMLPS DKHRIDTLWM SESGVVDLTF FIGPGPKDVL  
351 RQYTSVTGRP SMPQLFATAY HQCRWNYRDE EDVYNVDSKF DEHDIPYDVL  
401 WLDIEHTDGK KYFTWDRVLF PNPEEMQKKL AAKGRHMTI VDPHIKRDES  
451 YHIPKEALEK GYYVKDATGK DYDGCWCPGS SSYTDLLNPE IKSWWSDKFS  
501 LDSYVGSTKY LYIWNMNEP SVFNGPEVTM PRDALHHGGV EHRELHNSYG  
551 YYFHMGTSDG LLKRGDGKDR PFVLARAFFA GSQRYGAIWT GDNTAEWEHL  
601 RVSVPMVLTL SISGIVFSGA DVGGFNGNPD TELLVRWYQV GAYYPFFRGH  
651 AHHDTKRREP WLFGERNTQL MREAIHVRYM YLPYFYTLFR EANSSTGPVA  
701 RPLWMEFPGD EKSFSNDEAF MVGNGLLVQG VYTEKPKHVS VYLPGEESWY  
751 DLRSASAYNG GHTHKYEVS DSIPSFQRAG TIIPRKDRRL RSSTQMENDP  
801 YTLVIALNSS KAAEGELYID DGKSYEFKQG AFILKWEAYT FQMOPRLQLA  
851 VTHFPSECTV ERIILLGLSP GAKTALIEPG NKKVEIELGP LFIQGNRGSV  
901 PTIRKPNVRI TDDWSIQIL

FIG. 2.



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pot	1	.....MRAPLLLYPLLLLLLFTV...SAYSWKKE	25
hum	1	MGVRHPPCSHRLLAVALVSLATAALLGHILLHDFLLVPRELSGSSPVLE	50
pot	27	EFNRCDQTPFCKRARSRKPGSCNLRVADVSI SDGDLIAKLVPEENPESE	76
hum	51	ETHPAHQQGASRPGPRDAQAHGPRPRAVPTQCDVPPNSRFDCA PDKAITQ	100
pot	77	QPNKPLVLTLSVYQDGVMRVKIDEDQNLNP...PKKRFEVPEVIEEDFLN	123
hum	101	EQCEARGCCYIPAKQGLQGAQMGPWCFFPPSYPSYKLENLSSSEMGYTA	150
pot	124	TKLWLTR.....VKEEQIDGVSSFSSVFYLS DGYEGVLRHD.PFEV FAR	166
hum	151	TLTRTTPTFFPKDILT LRLDVMETENRLHFTIKDPANRRYEVPLETPRV	200
pot	167	ESGSGKRVLSIN.SNGLFD FEQLREKKEGDDWEEKFRSHTDTRP...YGPQ	213
hum	201	HSRAPSPLYSVEFSEEPFGVIVHR.....QLDGRVLLNTTVAPLFFADQ	244
pot	214	SISFDVSFYGADFVYGIPEHATSFALKPTKGP NVEEYSEPYRLFNL D VFE	263
hum	245	FLQLSTSL.PSOYITGLAEHLSPMLSTS.....WTRITLWNRDL..	283
pot	264	YLHESPFGLYGSIPFMISHGKARGSSGFFWL NAAEMQIDVLGSGWNSDES	313
hum	284	.APTFGANLYGSHPFYLALEDGGSAGVFL LNSNAMDVVLQPS PALS...	329
pot	314	SKIMLP SDKHRIDTLWMSESGVVD TFFF IGPGPKDVVRQYTSVTGRPSMP	363
hum	330	.....WRSTGGILDVYIFLGPEPKSVVQQYLDVVGYPFMP	364
pot	364	QLFATAYHQCRWNYRDEEDVYNVDSKFDEHD IPYDVLWLDIEHTDGKKYF	413
hum	365	PYWGLGFHL CRWGYSSTAITRQVENMTRAHFLDVQWNDLDYMDSR RDF	414
pot	414	TWDRVLF PNPEEMQKKLAAGRHMTIVDPHIK...RDESYHIPKEALEK	460
hum	415	TFNKDGF RDFFPAMVQELHQGGRRYMMIVDPAISSSGPAGSYR PYDEGLRR	464
pot	461	GYVVKDATGKDYGWCWPGSSSYTDLLNPEI KSWWSDKFSLDSYVGSTKY	510
hum	465	GVFITNETGQPLIGKVWPGSTAFPDFTNPTALAWWEDM..VAEFHDQVPF	512
pot	511	LYIWNDMNEPSVF.NGPEVTMPRDALHHGG.....	539
hum	513	DGMWIDMNEPSNFIRGSEDGCPNNELENPPYVPGVVG GTLQAATICASSH	562

FIG. 3.

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pot	540	...VEHRELHNSYGYFFHMGTS DGLLKRGDGKDRPFVLARAFFAGSORYG	586
hum	563	QFLSTHYNLHNLGLTEAIAASHRALVKARGT...RPFVISRSTFAGHGRYA	610
pot	587	AIWTGDNTAEWEHLRVSVPMVLTLSISGIVFSGADVGGFFGNPDTELLVR	636
hum	611	GHWTGDVWSSWEQLASSVPEILOFNLLGVPLVGADVCGFLGNTSEELCVR	660
pot	637	WYQVGAYYPFFRGHAHHDTKRREPWLFGERN TQLMREAIHVRMYLPHYFY	686
hum	661	WTQLGAFYPFMRNHNSLLSLPQEPYSFSEPAQQAMRKALTLRYALLPHLY	710
pot	687	TLFREANSSGTPVARPLWMEFPGDEKSF SNDEAFMVGNGLLVQGVYTEKP	736
hum	711	TLFHQAHVAGETVARPLFLEFPKDSSTWTVDHQLLWGEALLITPVLQAGK	750
pot	737	KHVSVYLPGEESWYDL.....RSASAYNGGHTHKYEV	768
hum	761	AEVTGYFP.LGTWYDLQTVPIEALGSLPPPPAAPREPAIHSEGQWVTLPA	809
pot	769	SEDSIPSFQAGTIIIPRKDLRRSSTQMENDPYTLVIALNSSKAAEGELY	818
hum	810	PLDTINVHLRAGYIIPLOGP.GLTTTESRQQPMALAVALTKGGEARGELF	858
pot	819	IDDGKSYEFKQGAFILKWEAYIFQMOPRLQLAVTHFPSECTVERIILLGL	868
hum	859	WDDGESLE.....VLERGAY.....TQVIFLAR	881
pot	869	SPGAKTALIEPGNKKVEIELGPLFIQGNRGSVPTIRKPNVRITDDWSIQI	918
hum	882	NNTIVNELVRVTSEGAGLQLOKQTVLG....VATAPO.....QV	916
pot	919	L*	
hum	917	LSNGVPVSNFTYSPDTKVLDCVSLLMGEQFLVSWC.....	952

FIG. 3 contd.

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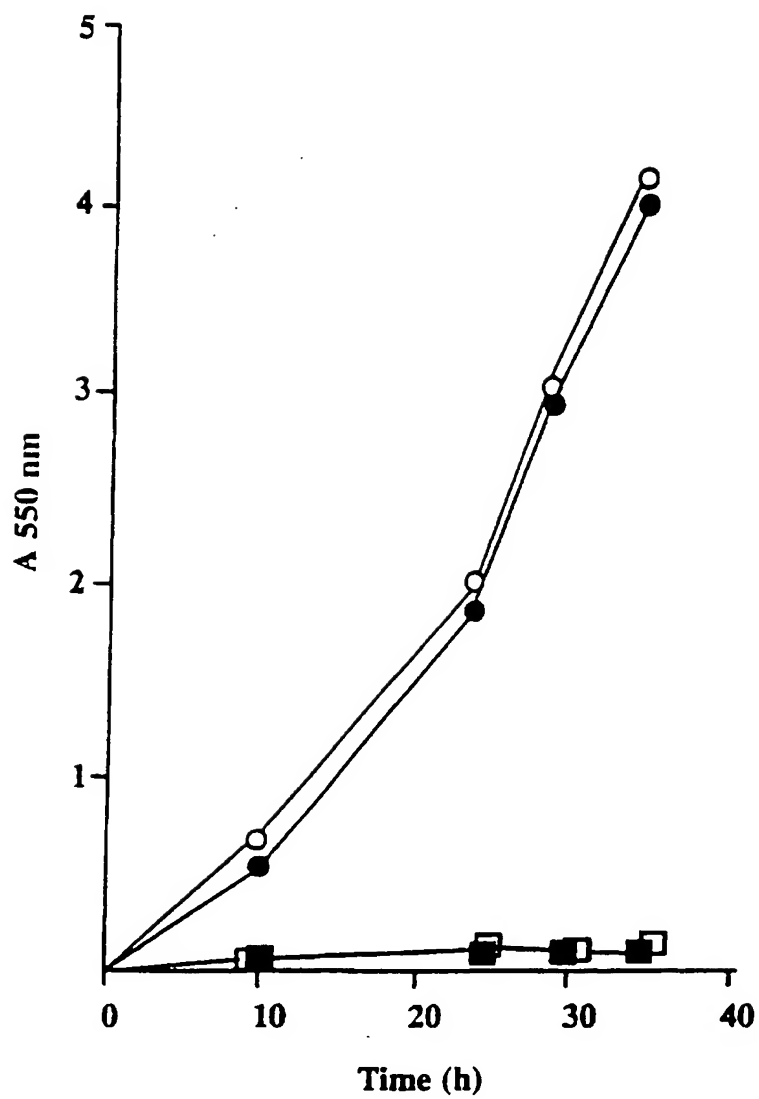


FIG. 4.

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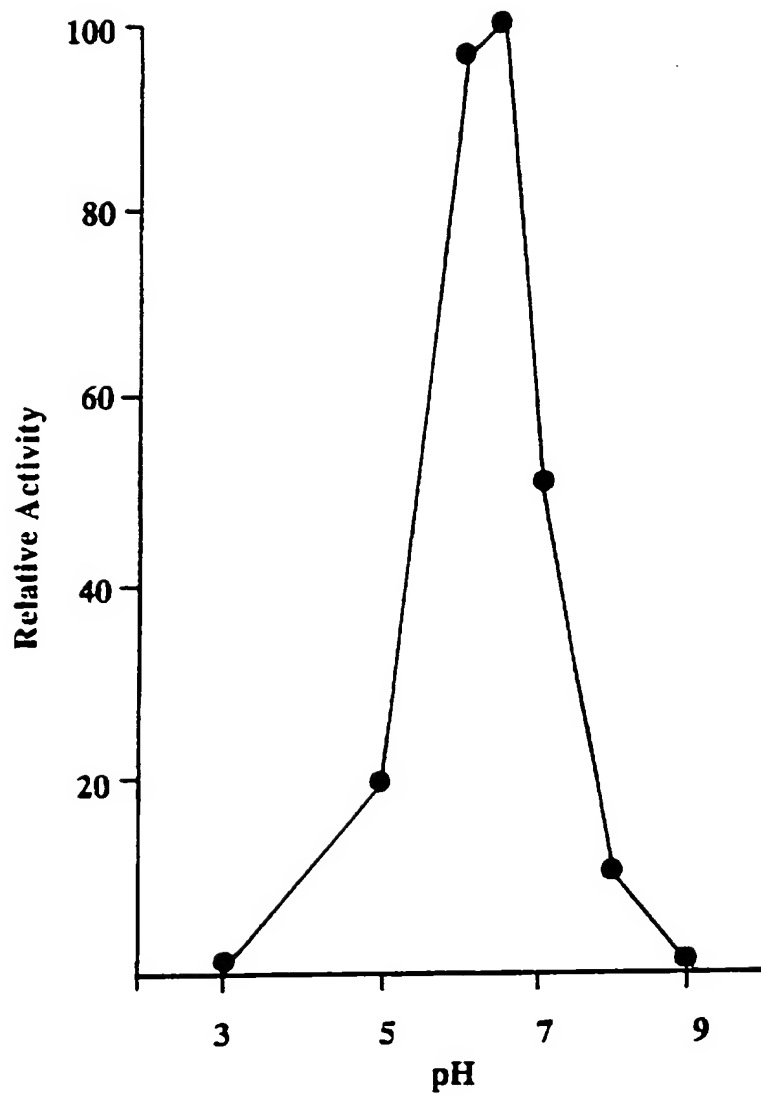


FIG. 5.

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/GB 96/03239

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N15/55 C12N1/21 C12N1/18 C12N5/10  
A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DE 42 13 444 A (INST GENBIOLOGISCHE FORSCHUNG) 28 October 1993  see column 3, line 9 - line 41; claims 1-3 ---	1,6,11, 16,17, 19, 21-28, 32-34
X	EMBL SEQUENCE DATABASE, REL. 44, 17-AUG-1995, ACCESSION NO. U22450, XP002029013 TIBBOT, B.K., ET AL.: "Hordeum vulgare alpha-glucosidase mRNA, complete cds." see sequence ---	1,5,9, 11,15, 17,21-25
X	GB 2 247 238 A (GUINNESS SON & CO LTD A) 26 February 1992  see the whole document ---	1,5,6, 9-11,19, 21-29
-/--		

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

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Date of the actual completion of the international search

8 April 1997

Date of mailing of the international search report

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# INTERNATIONAL SEARCH REPORT

Int:      nal Application No  
PCT/GB 96/03239

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International Application No

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